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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/495,448

DATE: 02/23/2000
TIME: 13:12:32

Input Set: I495448.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

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1 <110> APPLICANT: LAU, Lester F.
2 <120> TITLE OF INVENTION: EXTRACELLULAR MATRIX SIGNALLING MOLECULES
3 <130> FILE REFERENCE: 28758/36072
4 <140> CURRENT APPLICATION NUMBER: US/09/495,448
5 <141> CURRENT FILING DATE: 2000-01-31
6 <150> EARLIER APPLICATION NUMBER: 09/142,569
7 <151> EARLIER FILING DATE: 1999-04-02
8 <150> EARLIER APPLICATION NUMBER: 60/013,958
9 <151> EARLIER FILING DATE: 1996-03-15
10 <160> NUMBER OF SEQ ID NOS: 32
11 <170> SOFTWARE: PatentIn Ver. 2.0
12 <210> SEQ ID NO 1
13 <211> LENGTH: 1480
14 <212> TYPE: DNA
15 <213> ORGANISM: Mus musculus
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18 <222> LOCATION: (180)..(1316)
19 <220> FEATURE:
20 <223> OTHER INFORMATION: Mouse cyr61 cDNA coding sequence
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24      ctgcggggt tgttggttct gtgtcgccgc gctcgcccg gttctctctg cgcgccaca 179
25      atg agc tcc agc acc ttc agg acg ctc gct gtc gcc gtc acc ctt ctc 227
26      Met Ser Ser Ser Thr Phe Arg Thr Leu Ala Val Ala Val Thr Leu Leu
27      1          5          10          15
28      cac ttg acc aga ctg gcg ctc tcc acc tgc ccc gcc gcc tgc cac tgc 275
29      His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
30      20          25          30
31      cct ctg gag gca ccc aag tgc gcc ccg gga gtc ggg ttg gtc cgg gac 323
32      Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
33      35          40          45
34      ggc tgc ggc tgc tgt aag tgc tgc gct aaa caa ctc aac gag gac tgc 371
35      Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
36      50          55          60
37      agc aaa act cag ccc tgc gac cac acc aag ggg ttg gaa tgc aat ttc 419
38      Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
39      65          70          75          80
40      ggc gcc agc tcc acc gct ctg aaa ggg atc tgc aga gct cag tca gaa 467
41      Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
42      85          90          95
43      ggc aga ccc tgt gaa tat aac tcc aga atc tac caa aac ggg gaa agc 515
44      Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
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48			115				120	
49	ggc	tgc	att	cct	ctg	tgt	ccc	caa
50	Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln
51		130				135		140
52	tgt	ccc	aac	ccc	cgg	ctg	gtg	aaa
53	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys
54	145				150			155
55	tgg	gtt	tgt	gat	gaa	gac	agc	att
56	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile
57			165				170	
58	gac	ctc	ctc	gga	ctc	gat	gcc	tcg
59	Asp	Leu	Leu	Gly	Leu	Asp	Ala	Ser
60			180				185	
61	gag	tta	atc	gca	att	gga	aaa	ggc
62	Glu	Leu	Ile	Ala	Ile	Gly	Lys	Gly
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64	ttt	ggc	acc	gaa	ccg	cga	gtt	ctt
65	Phe	Gly	Thr	Glu	Pro	Arg	Val	Leu
66		210				215		220
67	cag	aaa	tgc	atc	gtt	cag	acc	acg
68	Gln	Lys	Cys	Ile	Val	Gln	Thr	Thr
69	225				230			235
70	tgc	gga	act	ggc	atc	tcc	aca	cga
71	Cys	Gly	Thr	Gly	Ile	Ser	Thr	Arg
72			245				250	
73	cgc	ctg	gtg	aaa	gag	acc	cgg	atc
74	Arg	Leu	Val	Lys	Glu	Thr	Arg	Ile
75			260				265	
76	cca	gtg	tac	agc	agc	cta	aaa	aag
77	Pro	Val	Tyr	Ser	Ser	Leu	Lys	Lys
78			275				280	
79	aaa	tcc	cca	gaa	cca	gtc	aga	ttt
80	Lys	Ser	Pro	Glu	Pro	Val	Arg	Phe
81		290				295		300
82	aag	aaa	tac	cgg	ccc	aaa	tac	tgc
83	Lys	Lys	Tyr	Arg	Pro	Lys	Tyr	Cys
84	305				310			315
85	tgc	aca	cct	ctg	cag	acc	aga	act
86	Cys	Thr	Pro	Leu	Gln	Thr	Arg	Thr
87			325				330	
88	gat	gga	gag	atg	ttt	tcc	aag	aat
89	Asp	Gly	Glu	Met	Phe	Ser	Lys	Asn
90			340				345	
91	tgt	aac	tac	aac	tgc	ccg	cat	ccc
92	Cys	Asn	Tyr	Asn	Cys	Pro	His	Pro
93		355					360	
94	agc	cta	ttc	aat	gac	atc	cac	aag

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98      aatgggtgct tgctcattct tgagtagcat tagggatttt caaaactgcc aaggggctga 1456
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108     20                      25                      30
109     Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg Asp
110     35                      40                      45
111     Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp Cys
112     50                      55                      60
113     Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn Phe
114     65                      70                      75                      80
115     Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser Glu
116     85                      90                      95
117     Gly Arg Pro Cys Glu Tyr Asn Ser Arg Ile Tyr Gln Asn Gly Glu Ser
118     100                     105                     110
119     Phe Gln Pro Asn Cys Lys His Gln Cys Thr Cys Ile Asp Gly Ala Val
120     115                     120                     125
121     Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu Gly
122     130                     135                     140
123     Cys Pro Asn Pro Arg Leu Val Lys Val Ser Gly Gln Cys Cys Glu Glu
124     145                     150                     155                     160
125     Trp Val Cys Asp Glu Asp Ser Ile Lys Asp Ser Leu Asp Asp Gln Asp
126     165                     170                     175
127     Asp Leu Leu Gly Leu Asp Ala Ser Glu Val Glu Leu Thr Arg Asn Asn
128     180                     185                     190
129     Glu Leu Ile Ala Ile Gly Lys Gly Ser Ser Leu Lys Arg Leu Pro Val
130     195                     200                     205
131     Phe Gly Thr Glu Pro Arg Val Leu Phe Asn Pro Leu His Ala His Gly
132     210                     215                     220
133     Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser Lys Ser
134     225                     230                     235                     240
135     Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro Glu Cys
136     245                     250                     255
137     Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys Gly Gln
138     260                     265                     270
139     Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys
140     275                     280                     285
141     Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Ser Ser Val
142     290                     295                     300
143     Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys
144     305                     310                     315                     320

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148                      340                      345                      350
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156 <213> ORGANISM: Homo sapiens
157 <220> FEATURE:
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159 <222> LOCATION: (124)..(1266)
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165      aca atg agc tcc cgc atc gcc agg gcg ctc gcc tta gtc gtc acc ctt 168
166      Met Ser Ser Arg Ile Ala Arg Ala Leu Ala Leu Val Val Thr Leu
167      1 5 10 15
168      ctc cac ttg acc agg ctg gcg ctc tcc acc tgc ccc gct gcc tgc cac 216
169      Leu His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His
170      20 25 30
171      tgc ccc ctg gag gcg ccc aag tgc gcg ccg gga gtc ggg ctg gtc cgg 264
172      Cys Pro Leu Glu Ala Pro Lys Cys Ala Pro Gly Val Gly Leu Val Arg
173      35 40 45
174      gac ggc tgc ggc tgc tgt aag tgc tgc gcc aag cag ctc aac gag gac 312
175      Asp Gly Cys Gly Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp
176      50 55 60
177      tgc agc aaa acg cag ccc tgc gac cac acc aag ggg ctg gaa tgc aac 360
178      Cys Ser Lys Thr Gln Pro Cys Asp His Thr Lys Gly Leu Glu Cys Asn
179      65 70 75
180      ttc ggc gcc agc tcc acc gct ctg aag ggg atc tgc aga gct cag tca 408
181      Phe Gly Ala Ser Ser Thr Ala Leu Lys Gly Ile Cys Arg Ala Gln Ser
182      80 85 90 95
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185      100 105 110
186      agt ttc cag ccc aac tgt caa cat cag tgc aca tgt att gat ggc gcc 504
187      Ser Phe Gln Pro Asn Cys Gln His Gln Cys Thr Cys Ile Asp Gly Ala
188      115 120 125
189      gtg ggc tgc att cct ctg tgt ccc caa gaa cta tct ctc ccc aac ttg 552
190      Val Gly Cys Ile Pro Leu Cys Pro Gln Glu Leu Ser Leu Pro Asn Leu
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199      Asp Gly Leu Leu Gly Lys Glu Leu Gly Phe Asp Ala Ser Glu Val Glu
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201      ttg acg aga aac aat gaa ttg att gca gtt gga aaa ggc aga tca ctg      744
202      Leu Thr Arg Asn Asn Glu Leu Ile Ala Val Gly Lys Gly Arg Ser Leu
203                      195                      200                      205
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205      Lys Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro
206                      210                      215                      220
207      tta caa ggc cag aaa tgt att gtt caa aca act tca tgg tcc cag tgc      840
208      Leu Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys
209      225                      230                      235
210      tca aag acc tgt gga act ggt atc tcc aca cga gtt acc aat gac aac      888
211      Ser Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn
212      240                      245                      250                      255
213      cct gag tgc cgc ctt gtg aaa gaa acc cgg att tgt gag gtg cgg cct      936
214      Pro Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro
215                      260                      265                      270
216      tgt gga cag cca gtg tac agc agc ctg aaa aag ggc aag aaa tgc agc      984
217      Cys Gly Gln Pro Val Tyr Ser Ser Leu Lys Lys Gly Lys Lys Cys Ser
218                      275                      280                      285
219      aag acc aag aaa tcc ccc gaa cca gtc agg ttt act tac gct gga tgt      1032
220      Lys Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys
221      290                      295                      300
222      ttg agt gtg aag aaa tac cgg ccc aag tac tgc ggt tcc tgc gtg gac      1080
223      Leu Ser Val Lys Lys Tyr Arg Pro Lys Tyr Cys Gly Ser Cys Val Asp
224      305                      310                      315
225      ggc cga tgc tgc acg ccc cag ctg acc agg act gtg aag atg cgg ttc      1128
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227      320                      325                      330                      335
228      cgc tgc gaa gat ggg gag aca ttt tcc aag aac gtc atg atg atc cag      1176
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232      Ser Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe
233      355                      360                      365
234      ccc ttc tac agg ctg ttc aat gac att cac aaa ttt agg gac      1266
235      Pro Phe Tyr Arg Leu Phe Asn Asp Ile His Lys Phe Arg Asp
236      370                      375                      380
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VERIFICATION SUMMARY
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DATE: 02/23/2000
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Line ? Error/Warning

Original Text

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